

Kouhei Tsumoto

List of Publications by Citations

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199
papers

4,321
citations

33
h-index

59
g-index

220
ext. papers

5,074
ext. citations

5.5
avg. IF

5.5
L-index

#	Paper	IF	Citations
199	Role of arginine in protein refolding, solubilization, and purification. <i>Biotechnology Progress</i> , 2004 , 20, 1301-8	2.8	327
198	Practical considerations in refolding proteins from inclusion bodies. <i>Protein Expression and Purification</i> , 2003 , 28, 1-8	2	324
197	Fucose depletion from human IgG1 oligosaccharide enhances binding enthalpy and association rate between IgG1 and Fcγ3R1a. <i>Journal of Molecular Biology</i> , 2004 , 336, 1239-49	6.5	280
196	Highly efficient recovery of functional single-chain Fv fragments from inclusion bodies overexpressed in <i>Escherichia coli</i> by controlled introduction of oxidizing reagent—application to a human single-chain Fv fragment. <i>Journal of Immunological Methods</i> , 1998 , 219, 119-29	2.5	176
195	Effects of acid exposure on the conformation, stability, and aggregation of monoclonal antibodies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 66, 954-62	4.2	149
194	Structural basis for self-assembly of a cytolytic pore lined by protein and lipid. <i>Nature Communications</i> , 2015 , 6, 6337	17.4	142
193	Open sandwich ELISA: a novel immunoassay based on the interchain interaction of antibody variable region. <i>Nature Biotechnology</i> , 1996 , 14, 1714-8	44.5	135
192	Arginine as an effective additive in gel permeation chromatography. <i>Journal of Chromatography A</i> , 2005 , 1094, 49-55	4.5	123
191	Solubilization of active green fluorescent protein from insoluble particles by guanidine and arginine. <i>Biochemical and Biophysical Research Communications</i> , 2003 , 312, 1383-6	3.4	121
190	Next generation drying technologies for pharmaceutical applications. <i>Journal of Pharmaceutical Sciences</i> , 2014 , 103, 2673-2695	3.9	118
189	Structural basis for binding of human IgG1 to its high-affinity human receptor FcγR1. <i>Nature Communications</i> , 2015 , 6, 6866	17.4	87
188	Effects of salts on protein-surface interactions: applications for column chromatography. <i>Journal of Pharmaceutical Sciences</i> , 2007 , 96, 1677-90	3.9	71
187	Structural basis for multimeric heme complexation through a specific protein-heme interaction: the case of the third neat domain of IsdH from <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2008 , 283, 28649-59	5.4	67
186	Affinity improvement of a therapeutic antibody by structure-based computational design: generation of electrostatic interactions in the transition state stabilizes the antibody-antigen complex. <i>PLoS ONE</i> , 2014 , 9, e87099	3.7	65
185	Heme degradation by <i>Staphylococcus aureus</i> IsdG and IsdI liberates formaldehyde rather than carbon monoxide. <i>Biochemistry</i> , 2013 , 52, 3025-7	3.2	64
184	A secondary RET mutation in the activation loop conferring resistance to vandetanib. <i>Nature Communications</i> , 2018 , 9, 625	17.4	52
183	Arginine improves protein elution in hydrophobic interaction chromatography. The cases of human interleukin-6 and activin-A. <i>Journal of Chromatography A</i> , 2007 , 1154, 81-6	4.5	47

182	Catalytic activity of MsbA reconstituted in nanodisc particles is modulated by remote interactions with the bilayer. <i>FEBS Letters</i> , 2011 , 585, 3533-7	3.8	45
181	Structural analysis of Fc/FcR complexes: a blueprint for antibody design. <i>Immunological Reviews</i> , 2015 , 268, 201-21	11.3	43
180	Mapping ultra-weak protein-protein interactions between heme transporters of <i>Staphylococcus aureus</i> . <i>Journal of Biological Chemistry</i> , 2012 , 287, 16477-87	5.4	42
179	Effects of subclass change on the structural stability of chimeric, humanized, and human antibodies under thermal stress. <i>Protein Science</i> , 2013 , 22, 1542-51	6.3	40
178	Molecular basis of recognition of antibacterial porphyrins by heme-transporter IsdH-NEAT3 of <i>Staphylococcus aureus</i> . <i>Biochemistry</i> , 2011 , 50, 7311-20	3.2	40
177	Structures of the prefusion form of measles virus fusion protein in complex with inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 2496-2501	11.5	38
176	Structural basis for amino acid export by DMT superfamily transporter YddG. <i>Nature</i> , 2016 , 534, 417-20	50.4	38
175	Through-bond effects in the ternary complexes of thrombin sandwiched by two DNA aptamers. <i>Nucleic Acids Research</i> , 2017 , 45, 461-469	20.1	37
174	Bidirectional binding property of high glycine-tyrosine keratin-associated protein contributes to the mechanical strength and shape of hair. <i>Journal of Structural Biology</i> , 2013 , 183, 484-494	3.4	37
173	Signal peptide design for improving recombinant protein secretion in the baculovirus expression vector system. <i>Biochemical and Biophysical Research Communications</i> , 2010 , 391, 931-5	3.4	37
172	Osteomodulin regulates diameter and alters shape of collagen fibrils. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 463, 292-6	3.4	36
171	Expression of a model peptide of a marine mussel adhesive protein in <i>Escherichia coli</i> and characterization of its structural and functional properties. <i>Journal of Polymer Science Part A</i> , 1999 , 37, 729-736	2.5	36
170	Mutations for decreasing the immunogenicity and maintaining the function of core streptavidin. <i>Protein Science</i> , 2013 , 22, 213-21	6.3	35
169	Glycosylation of IgG-Fc: a molecular perspective. <i>International Immunology</i> , 2017 , 29, 311-317	4.9	34
168	The Atomic Structure of the HIV-1 gp41 Transmembrane Domain and Its Connection to the Immunogenic Membrane-proximal External Region. <i>Journal of Biological Chemistry</i> , 2015 , 290, 12999-30154	5.4	34
167	Dual-Sensitive Nanomicelles Enhancing Systemic Delivery of Therapeutically Active Antibodies Specifically into the Brain. <i>ACS Nano</i> , 2020 , 14, 6729-6742	16.7	33
166	Structure of the triose-phosphate/phosphate translocator reveals the basis of substrate specificity. <i>Nature Plants</i> , 2017 , 3, 825-832	11.5	31
165	Analysis of Pore Formation and Protein Translocation Using Large Biological Nanopores. <i>Analytical Chemistry</i> , 2017 , 89, 11269-11277	7.8	29

164	A pore-forming toxin requires a specific residue for its activity in membranes with particular physicochemical properties. <i>Journal of Biological Chemistry</i> , 2015 , 290, 10850-61	5.4	29
163	Thermodynamics of antibody-antigen interaction revealed by mutation analysis of antibody variable regions. <i>Journal of Biochemistry</i> , 2015 , 158, 1-13	3.1	29
162	A stable phage-display system using a phagemid vector: phage display of hen egg-white lysozyme (HEL), Escherichia coli alkaline phosphatase, and anti-HEL monoclonal antibody, HyHEL10. <i>Biochemical and Biophysical Research Communications</i> , 1996 , 218, 682-7	3.4	29
161	Assessing the Heterogeneity of the Fc-Glycan of a Therapeutic Antibody Using an engineered FcReceptor IIIa-Immobilized Column. <i>Scientific Reports</i> , 2018 , 8, 3955	4.9	27
160	Protective effect of the long pentraxin PTX3 against histone-mediated endothelial cell cytotoxicity in sepsis. <i>Science Signaling</i> , 2014 , 7, ra88	8.8	27
159	Peptide-dependent conformational fluctuation determines the stability of the human leukocyte antigen class I complex. <i>Journal of Biological Chemistry</i> , 2014 , 289, 24680-90	5.4	27
158	Repertoire Analysis of Antibody CDR-H3 Loops Suggests Affinity Maturation Does Not Typically Result in Rigidification. <i>Frontiers in Immunology</i> , 2018 , 9, 413	8.4	26
157	Tumor-directed lymphocyte-activating cytokines: refolding-based preparation of recombinant human interleukin-12 and an antibody variable domain-fused protein by additive-introduced stepwise dialysis. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 328, 98-105	3.4	25
156	Structural basis for broad neutralization of HIV-1 through the molecular recognition of 10E8 helical epitope at the membrane interface. <i>Scientific Reports</i> , 2016 , 6, 38177	4.9	25
155	Improving the affinity of an antibody for its antigen via long-range electrostatic interactions. <i>Protein Engineering, Design and Selection</i> , 2013 , 26, 773-80	1.9	24
154	Differential Effect of Membrane Composition on the Pore-Forming Ability of Four Different Sea Anemone Actinoporins. <i>Biochemistry</i> , 2016 , 55, 6630-6641	3.2	21
153	Structural and Thermodynamic Basis of Epitope Binding by Neutralizing and Nonneutralizing Forms of the Anti-HIV-1 Antibody 4E10. <i>Journal of Virology</i> , 2015 , 89, 11975-89	6.6	20
152	Immobilized oxidoreductase as an additive for refolding inclusion bodies: application to antibody fragments. <i>Protein Engineering, Design and Selection</i> , 2003 , 16, 535-41	1.9	20
151	Identification of a Membrane-bound Prepore Species Clarifies the Lytic Mechanism of Actinoporins. <i>Journal of Biological Chemistry</i> , 2016 , 291, 19210-19219	5.4	20
150	Engineering Stability, Viscosity, and Immunogenicity of Antibodies by Computational Design. <i>Journal of Pharmaceutical Sciences</i> , 2020 , 109, 1631-1651	3.9	19
149	Polymeric SpyCatcher Scaffold Enables Bioconjugation in a Ratio-Controllable Manner. <i>Biotechnology Journal</i> , 2017 , 12, 1700195	5.6	18
148	Exploring designability of electrostatic complementarity at an antigen-antibody interface directed by mutagenesis, biophysical analysis, and molecular dynamics simulations. <i>Scientific Reports</i> , 2019 , 9, 4482	4.9	18
147	Discovery and Optimization of Inhibitors of the Parkinson Disease Associated Protein DJ-1. <i>ACS Chemical Biology</i> , 2018 , 13, 2783-2793	4.9	18

146	Discovery and characterization of natural tropolones as inhibitors of the antibacterial target CapF from <i>Staphylococcus aureus</i> . <i>Scientific Reports</i> , 2015 , 5, 15337	4.9	18
145	Folding-unfolding of goat alpha-lactalbumin studied by stopped-flow circular dichroism and molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 42, 49-65	4.2	18
144	Phospholipid Membrane Fluidity Alters Ligand Binding Activity of a G Protein-Coupled Receptor by Shifting the Conformational Equilibrium. <i>Biochemistry</i> , 2019 , 58, 504-508	3.2	18
143	Design strategy for serine hydroxymethyltransferase probes based on retro-aldol-type reaction. <i>Nature Communications</i> , 2019 , 10, 876	17.4	17
142	Polymeric Nanocarriers with Controlled Chain Flexibility Boost mRNA Delivery In Vivo through Enhanced Structural Fastening. <i>Advanced Healthcare Materials</i> , 2020 , 9, e2000538	10.1	17
141	Selective binding of antimicrobial porphyrins to the heme-receptor IsdH-NEAT3 of <i>Staphylococcus aureus</i> . <i>Protein Science</i> , 2013 , 22, 942-53	6.3	17
140	Affinity Improvement of a Cancer-Targeted Antibody through Alanine-Induced Adjustment of Antigen-Antibody Interface. <i>Structure</i> , 2019 , 27, 519-527.e5	5.2	17
139	Use of SpyTag/SpyCatcher to construct bispecific antibodies that target two epitopes of a single antigen. <i>Journal of Biochemistry</i> , 2017 , 162, 203-210	3.1	16
138	Identification of key modules and hub genes for small-cell lung carcinoma and large-cell neuroendocrine lung carcinoma by weighted gene co-expression network analysis of clinical tissue-proteomes. <i>PLoS ONE</i> , 2019 , 14, e0217105	3.7	16
137	Functional characterization of Val60, a key residue involved in the membrane-oligomerization of fragaceatoxin C, an actinoporin from <i>Actinia fragacea</i> . <i>FEBS Letters</i> , 2015 , 589, 1840-6	3.8	16
136	Heme binding mechanism of structurally similar iron-regulated surface determinant near transporter domains of <i>Staphylococcus aureus</i> exhibiting different affinities for heme. <i>Biochemistry</i> , 2013 , 52, 8866-77	3.2	16
135	Improvement of antibody affinity by introduction of basic amino acid residues into the framework region. <i>Biochemistry and Biophysics Reports</i> , 2018 , 15, 81-85	2.2	15
134	A Peptoid with Extended Shape in Water. <i>Journal of the American Chemical Society</i> , 2019 , 141, 14612-14623	6.34	15
133	Dynamic elements govern the catalytic activity of CapE, a capsular polysaccharide-synthesizing enzyme from <i>Staphylococcus aureus</i> . <i>FEBS Letters</i> , 2013 , 587, 3824-30	3.8	15
132	Crystal structure of the capsular polysaccharide synthesizing protein CapE of <i>Staphylococcus aureus</i> . <i>Bioscience Reports</i> , 2013 , 33,	4.1	15
131	Replacing factor-dependency with that for lysozyme: affordable culture of IL-6-dependent hybridoma by transfecting artificial cell surface receptor. <i>Biotechnology and Bioengineering</i> , 2001 , 74, 416-23	4.9	15
130	Quantitative phosphoproteomics-based molecular network description for high-resolution kinase-substrate interactome analysis. <i>Bioinformatics</i> , 2016 , 32, 2083-8	7.2	15
129	Click conjugation of a binuclear terbium(III) complex for real-time detection of tyrosine phosphorylation. <i>Analytical Chemistry</i> , 2015 , 87, 3834-40	7.8	14

128	Alternative downstream processes for production of antibodies and antibody fragments. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 2032-2040	4	14
127	Bidirectional Transformation of a Metamorphic Protein between the Water-Soluble and Transmembrane Native States. <i>Biochemistry</i> , 2015 , 54, 6863-6	3.2	14
126	Incorporation of rapid thermodynamic data in fragment-based drug discovery. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 2155-9	8.3	14
125	Critical contribution of aromatic rings to specific recognition of polyether rings. The case of ciguatoxin CTX3C-ABC and its specific antibody 1C49. <i>Journal of Biological Chemistry</i> , 2008 , 283, 12259-66	5.4	14
124	Structural and thermodynamic basis for the recognition of the substrate-binding cleft on hen egg lysozyme by a single-domain antibody. <i>Scientific Reports</i> , 2019 , 9, 15481	4.9	14
123	Antibody Affinity Maturation by Computational Design. <i>Methods in Molecular Biology</i> , 2018 , 1827, 15-34	1.4	14
122	PRDM14 directly interacts with heat shock proteins HSP90 α and glucose-regulated protein 78. <i>Cancer Science</i> , 2018 , 109, 373-383	6.9	13
121	Integrative Network Analysis Combined with Quantitative Phosphoproteomics Reveals Transforming Growth Factor-beta Receptor type-2 (TGFBR2) as a Novel Regulator of Glioblastoma Stem Cell Properties. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1017-31	7.6	13
120	Efficacy of ribavirin against malignant glioma cell lines. <i>Oncology Letters</i> , 2014 , 8, 2469-2474	2.6	13
119	Contributions of interfacial residues of human Interleukin15 to the specificity and affinity for its private alpha-receptor. <i>Journal of Molecular Biology</i> , 2009 , 389, 880-94	6.5	13
118	Assessment of the Protein-Protein Interactions in a Highly Concentrated Antibody Solution by Using Raman Spectroscopy. <i>Pharmaceutical Research</i> , 2016 , 33, 956-69	4.5	13
117	Thermodynamic and computational analyses reveal the functional roles of the galloyl group of tea catechins in molecular recognition. <i>PLoS ONE</i> , 2018 , 13, e0204856	3.7	13
116	Disruption of cell adhesion by an antibody targeting the cell-adhesive intermediate (X-dimer) of human P-cadherin. <i>Scientific Reports</i> , 2017 , 7, 39518	4.9	12
115	Identification and characterization of the X-dimer of human P-cadherin: implications for homophilic cell adhesion. <i>Biochemistry</i> , 2014 , 53, 1742-52	3.2	12
114	Elucidation of potential sites for antibody engineering by fluctuation editing. <i>Scientific Reports</i> , 2017 , 7, 9597	4.9	12
113	The staphylococcal elastin-binding protein regulates zinc-dependent growth/biofilm formation. <i>Journal of Biochemistry</i> , 2014 , 156, 155-62	3.1	12
112	Functional Contacts between MPER and the Anti-HIV-1 Broadly Neutralizing Antibody 4E10 Extend into the Core of the Membrane. <i>Journal of Molecular Biology</i> , 2017 , 429, 1213-1226	6.5	11
111	Crystal structure of streptavidin mutant with low immunogenicity. <i>Journal of Bioscience and Bioengineering</i> , 2015 , 119, 642-7	3.3	11

110	Molecular basis for governing the morphology of type-I collagen fibrils by Osteomodulin. <i>Communications Biology</i> , 2018 , 1, 33	6.7	11
109	Non-core region modulates interleukin-11 signaling activity: generation of agonist and antagonist variants. <i>Journal of Biological Chemistry</i> , 2011 , 286, 8085-8093	5.4	10
108	Contribution of Thr29 to the thermodynamic stability of goat alpha-lactalbumin as determined by experimental and theoretical approaches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 16-29	4.2	10
107	Peripheral Membrane Interactions Boost the Engagement by an Anti-HIV-1 Broadly Neutralizing Antibody. <i>Journal of Biological Chemistry</i> , 2017 , 292, 5571-5583	5.4	9
106	Epiregulin Recognition Mechanisms by Anti-epiregulin Antibody 9E5: STRUCTURAL, FUNCTIONAL, AND MOLECULAR DYNAMICS SIMULATION ANALYSES. <i>Journal of Biological Chemistry</i> , 2016 , 291, 2319-30	5.4	9
105	Rapid Heme Transfer Reactions between NEAr Transporter Domains of Staphylococcus aureus: A Theoretical Study Using QM/MM and MD Simulations. <i>PLoS ONE</i> , 2015 , 10, e0145125	3.7	9
104	Crystal structure of the enzyme CapF of Staphylococcus aureus reveals a unique architecture composed of two functional domains. <i>Biochemical Journal</i> , 2012 , 443, 671-80	3.8	9
103	Step-wise refolding of recombinant proteins. <i>Current Pharmaceutical Biotechnology</i> , 2010 , 11, 285-8	2.6	9
102	Structural and thermodynamic characterization of the self-adhesive properties of human P-cadherin. <i>Molecular BioSystems</i> , 2012 , 8, 2050-3		8
101	Stepwise characterization of the thermodynamics of trichocyte intermediate filament protein supramolecular assembly. <i>Journal of Molecular Biology</i> , 2011 , 408, 832-8	6.5	8
100	Adhesive Dimerization of Human P-Cadherin Catalyzed by a Chaperone-like Mechanism. <i>Structure</i> , 2016 , 24, 1523-36	5.2	8
99	Haemolytic actinoporins interact with carbohydrates using their lipid-binding module. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	7
98	Generation and characterization of antagonistic anti-human interleukin (IL)-18 monoclonal antibodies with high affinity: Two types of monoclonal antibodies against full-length IL-18 and the neoepitope of inflammatory caspase-cleaved active IL-18. <i>Archives of Biochemistry and Biophysics</i> , 2019 , 663, 71-82	4.1	7
97	Discovery of chemical probes that suppress Wnt/Ecatenin signaling through high-throughput screening. <i>Cancer Science</i> , 2020 , 111, 783-794	6.9	7
96	Intramolecular H-bonds govern the recognition of a flexible peptide by an antibody. <i>Journal of Biochemistry</i> , 2018 , 164, 65-76	3.1	7
95	A combination of F NMR and surface plasmon resonance for site-specific hit selection and validation of fragment molecules that bind to the ATP-binding site of a kinase. <i>Bioorganic and Medicinal Chemistry</i> , 2018 , 26, 1929-1938	3.4	7
94	The Isolation of New Pore-Forming Toxins from the Sea Anemone Provides Insights into the Mechanisms of Actinoporin Evolution. <i>Toxins</i> , 2019 , 11,	4.9	7
93	The carboxyl-terminal region of Dok-7 plays a key, but not essential, role in activation of muscle-specific receptor kinase MuSK and neuromuscular synapse formation. <i>Journal of Biochemistry</i> , 2017 , 161, 269-277	3.1	7

92	Inhibition of hepatitis C virus NS3 protease by peptides derived from complementarity-determining regions (CDRs) of the monoclonal antibody 8D4: tolerance of a CDR peptide to conformational changes of a target. <i>FEBS Letters</i> , 2002 , 525, 77-82	3.8	7
91	Per-Residue Program of Multiple Backbone Dihedral Angles of β Peptoids via Backbone Substitutions. <i>Journal of the American Chemical Society</i> , 2020 , 142, 2277-2284	16.4	7
90	Tyrosine Sulfation Restricts the Conformational Ensemble of a Flexible Peptide, Strengthening the Binding Affinity for an Antibody. <i>Biochemistry</i> , 2018 , 57, 4177-4185	3.2	7
89	System-Wide Analysis of Protein Acetylation and Ubiquitination Reveals a Diversified Regulation in Human Cancer Cells. <i>Biomolecules</i> , 2020 , 10,	5.9	6
88	Differential binding of prohibitin-2 to estrogen receptor α and to drug-resistant ER α mutants. <i>Biochemical and Biophysical Research Communications</i> , 2015 , 463, 726-31	3.4	6
87	Functional Fv fragment of an antibody specific for CD28: Fv-mediated co-stimulation of T cells. <i>FEBS Letters</i> , 2000 , 476, 266-71	3.8	6
86	Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics.. <i>MAbs</i> , 2022 , 14, 2020082	6.6	6
85	Structural Basis for the Binding Mechanism of Human Serum Albumin Complexed with Cyclic Peptide Dalbavancin. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 14045-14053	8.3	6
84	An epitope-directed antibody affinity maturation system utilizing mammalian cell survival as readout. <i>Biotechnology and Bioengineering</i> , 2019 , 116, 1742-1751	4.9	5
83	Differential Effects of IFN- β on the Survival and Growth of Human Vascular Smooth Muscle and Endothelial Cells. <i>BioResearch Open Access</i> , 2015 , 4, 1-15	2.4	5
82	Generation of biparatopic antibody through two-step targeting of fragment antibodies on antigen using SpyTag and SpyCatcher. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2020 , 25, e00418	5.3	5
81	Characterization of glycoengineered anti-HER2 monoclonal antibodies produced by using a silkworm-baculovirus expression system. <i>Journal of Biochemistry</i> , 2018 , 163, 481-488	3.1	5
80	How the protonation state of a phosphorylated amino acid governs molecular recognition: insights from classical molecular dynamics simulations. <i>FEBS Letters</i> , 2020 , 594, 903-912	3.8	5
79	Structure-based design and discovery of novel anti-tissue factor antibodies with cooperative double-point mutations, using interaction analysis. <i>Scientific Reports</i> , 2020 , 10, 17590	4.9	5
78	Structural basis for antigen recognition by methylated lysine-specific antibodies. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100176	5.4	5
77	Apoptotic Cell-Inspired Polymeric Particles for Controlling Microglial Inflammation toward Neurodegenerative Disease Treatment. <i>ACS Biomaterials Science and Engineering</i> , 2019 , 5, 5705-5713	5.5	4
76	Synergistic Cytotoxic Effect on Gastric Cancer Cells of an Immunotoxin Cocktail in Which Antibodies Recognize Different Epitopes on CDH17. <i>Monoclonal Antibodies in Immunodiagnosis and Immunotherapy</i> , 2018 , 37, 1-11	1.9	4
75	Inhibition of homophilic dimerization and disruption of cell adhesion by P-cadherin-specific small molecules from SPR-based assays. <i>Chemical Communications</i> , 2018 , 54, 5350-5353	5.8	4

74	Structural basis for binding and transfer of heme in bacterial heme-acquisition systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017 , 85, 2217-2230	4.2	4
73	Expression, purification, crystallization and preliminary diffraction analysis of CapF, a capsular polysaccharide-synthesis enzyme from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008 , 64, 512-5		4
72	Structural and thermodynamical insights into the binding and inhibition of FIH-1 by the N-terminal disordered region of Mint3. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101304	5.4	4
71	A new twist of rubredoxin function in <i>M. tuberculosis</i> . <i>Bioorganic Chemistry</i> , 2021 , 109, 104721	5.1	4
70	In-labeled anti-cadherin17 antibody D2101 has potential as a noninvasive imaging probe for diagnosing gastric cancer and lymph-node metastasis. <i>Annals of Nuclear Medicine</i> , 2020 , 34, 13-23	2.5	4
69	Elaboration of Non-naturally Occurring Helical Tripeptides as p53-MDM2/MDMX Interaction Inhibitors. <i>Chemical and Pharmaceutical Bulletin</i> , 2021 , 69, 681-692	1.9	4
68	Roles of the disulfide bond between the variable and the constant domains of rabbit immunoglobulin kappa chains in thermal stability and affinity. <i>Protein Engineering, Design and Selection</i> , 2018 , 31, 243-247	1.9	3
67	Biophysical characterization of the interaction between heme and proteins responsible for heme transfer in <i>Streptococcus pyogenes</i> . <i>Biochemical and Biophysical Research Communications</i> , 2017 , 493, 1109-1114	3.4	3
66	Manipulation of protein-complex function by using an engineered heterotrimeric coiled-coil switch. <i>Organic and Biomolecular Chemistry</i> , 2009 , 7, 3102	3.9	3
65	Relationship between Fluorescence Intensity of GFP and the Expression Level of Prestin in a Prestin-Expressing Chinese Hamster Ovary Cell Line. <i>JSME International Journal Series C-Mechanical Systems Machine Elements and Manufacturing</i> , 2004 , 47, 970-976		3
64	Antigen-Mediated Genetically Modified Cell Amplification (AMEGA) with Single Vector Transduction. <i>Journal of Chemical Engineering of Japan</i> , 2004 , 37, 1259-1264	0.8	3
63	Structure-based screening combined with computational and biochemical analyses identified the inhibitor targeting the binding of DNA Ligase 1 to UHRF1. <i>Bioorganic and Medicinal Chemistry</i> , 2021 , 52, 116500	3.4	3
62	Delicate balance among thermal stability, binding affinity, and conformational space explored by single-domain VH antibodies. <i>Scientific Reports</i> , 2021 , 11, 20624	4.9	3
61	A DNA Aptamer That Inhibits the Aberrant Signaling of Fibroblast Growth Factor Receptor in Cancer Cells. <i>Jacs Au</i> , 2021 , 1, 578-585		3
60	Heme controls the structural rearrangement of its sensor protein mediating the hemolytic bacterial survival. <i>Communications Biology</i> , 2021 , 4, 467	6.7	3
59	In-Cell Enzymology To Probe His-Heme Ligation in Heme Oxygenase Catalysis. <i>Biochemistry</i> , 2016 , 55, 4836-49	3.2	3
58	Effects of a remote mutation from the contact paratope on the structure of CDR-H3 in the anti-HIV neutralizing antibody PG16. <i>Scientific Reports</i> , 2019 , 9, 19840	4.9	3
57	Peptoid-based reprogrammable template for cell-permeable inhibitors of protein-protein interactions. <i>Chemical Science</i> , 2021 , 12, 13292-13300	9.4	3

56	A glutamine sensor that directly activates TORC1. <i>Communications Biology</i> , 2021 , 4, 1093	6.7	3
55	Control of Protein Adsorption to Cyclo Olefin Polymer by the Hofmeister Effect. <i>Journal of Pharmaceutical Sciences</i> , 2019 , 108, 1686-1691	3.9	2
54	Highly sensitive HPLC analysis and biophysical characterization of N-glycans of IgG-Fc domain in comparison between CHO and 293 cells using FcR1IIa ligand. <i>Biotechnology Progress</i> , 2020 , 36, e3016	2.8	2
53	Methodology for Further Thermostabilization of an Intrinsically Thermostable Membrane Protein Using Amino Acid Mutations with Its Original Function Being Retained. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 1709-1716	6.1	2
52	Development of drug discovery screening system by molecular interaction kinetics-mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2018 , 32, 665-671	2.2	2
51	Production and characterization of a novel site-specific-modifiable anti-OX40-receptor single-chain variable fragment for targeted drug delivery. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 496, 614-620	3.4	2
50	Reply to "The Broadly Neutralizing, Anti-HIV Antibody 4E10: an Open and Shut Case?". <i>Journal of Virology</i> , 2016 , 90, 3276-7	6.6	2
49	Long-Term Stability and Reversible Thermal Unfolding of Antibody Structure at Low pH: Case Study. <i>Journal of Pharmaceutical Sciences</i> , 2018 , 107, 2965-2967	3.9	2
48	Structural behavior of keratin-associated protein 8.1 in human hair as revealed by a monoclonal antibody. <i>Journal of Structural Biology</i> , 2018 , 204, 207-214	3.4	2
47	Production and characterization of genetically modified human IL-11 variants. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 205-217	4	2
46	Purification of the Motor Protein Prestin from Chinese Hamster Ovary Cells Stably Expressing Prestin. <i>Journal of Biomechanical Science and Engineering</i> , 2008 , 3, 221-234	0.8	2
45	Technical Capabilities and Limitations of Optical Spectroscopy and Calorimetry Using Water-Miscible Solvents: The Case of Dimethyl Sulfoxide, Acetonitrile, and 1,4-Dioxane. <i>Journal of Pharmaceutical Sciences</i> , 2020 , 109, 524-531	3.9	2
44	Unique Electronic Structures of the Highly Ruffled Hemes in Heme-Degrading Enzymes of , IsdG and IsdI, by Resonance Raman and Electron Paramagnetic Resonance Spectroscopies. <i>Biochemistry</i> , 2020 , 59, 3918-3928	3.2	2
43	Anti-EGFR antibody 528 binds to domain III of EGFR at a site shifted from the cetuximab epitope. <i>Scientific Reports</i> , 2021 , 11, 5790	4.9	2
42	A Novel Cell-Based Intracellular Protein-Protein Interaction Detection Platform (SOLIS) for Multimodality Screening. <i>ACS Synthetic Biology</i> , 2021 , 10, 990-999	5.7	2
41	Computer-guided library generation applied to the optimization of single-domain antibodies. <i>Protein Engineering, Design and Selection</i> , 2019 , 32, 423-431	1.9	2
40	Site-specific Manipulation of Mitochondrial DNA by Artificial Restriction DNA Cutter. <i>Chemistry Letters</i> , 2019 , 48, 1332-1335	1.7	1
39	Structural features of methionine aminopeptidase2-active core peptide essential for binding with S100A4. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 516, 1123-1129	3.4	1

38	Effect of allotypic variation of human IgG1 on the thermal stability of disulfide-linked knobs-into-holes mutants of the Fc for stable bispecific antibody design. <i>Antibody Therapeutics</i> , 2019 , 2, 65-69	5.8	1
37	Biophysical characterization of the breast cancer-related BIG3-PHB2 interaction: Effect of non-conserved loop region of BIG3 on the structure and the interaction. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 518, 183-189	3.4	1
36	Thermodynamic analyses of amino acid residues at the interface of an antibody B2212A and its antigen roundabout homolog 1. <i>Journal of Biochemistry</i> , 2017 , 162, 255-258	3.1	1
35	Structural basis for inhibition of the Tob-CNOT7 interaction by a fragment screening approach. <i>Protein and Cell</i> , 2015 , 6, 924-8	7.2	1
34	Solvent Interactions with Proteins and Other Macromolecules 2011 , 277-360		1
33	Functional Expression of Prestin, the Outer Hair Cell Motor Protein, Using the Baculovirus/Insect Cell System. <i>Journal of Biomechanical Science and Engineering</i> , 2008 , 3, 287-298	0.8	1
32	Effects of Mutation in the Conserved GTSRH Sequence of the Motor Protein Prestin on Its Characteristics. <i>JSME International Journal Series C-Mechanical Systems Machine Elements and Manufacturing</i> , 2005 , 48, 403-410		1
31	The transcriptional corepressor CtBP2 serves as a metabolite sensor orchestrating hepatic glucose and lipid homeostasis. <i>Nature Communications</i> , 2021 , 12, 6315	17.4	1
30	Development and activities, including immunocomplex formation, of biparatopic antibodies and alternative scaffold proteins. <i>Translational and Regulatory Sciences</i> , 2020 , 2, 1-6	0.3	1
29	Anion solvation enhanced by positive supercharging mutations preserves thermal stability of an antibody in a wide pH range. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 563, 54-59	3.4	1
28	Modified AMBER force-field (FUJI) parameters for sulfated and phosphorylated tyrosine residues: Development and application to CCR5-derived peptide systems 2019 ,		1
27	Proteomic identification and validation of novel interactions of the putative tumor suppressor PRELP with membrane proteins including IGF1-R and p75NTR. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100278	5.4	1
26	An integrated computational pipeline for designing high-affinity nanobodies with expanded genetic codes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	1
25	Molecular basis for the activation of actinoporins by lipids. <i>Methods in Enzymology</i> , 2021 , 649, 277-306	1.7	1
24	Experimental Comparison of Bond Lifetime and Viscoelastic Relaxation in Transient Networks with Well-Controlled Structures.. <i>ACS Macro Letters</i> , 2022 , 753-759	6.6	1
23	Development of biparatopic bispecific antibody possessing tetravalent scFv-Fc capable of binding to ROBO1 expressed in hepatocellular carcinoma cells. <i>Journal of Biochemistry</i> , 2021 , 170, 307-315	3.1	0
22	Thermodynamic Dissection of Potency and Selectivity of Cytosolic Hsp90 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 2669-2677	8.3	0
21	Characterization of a putative maltodextrin-binding protein of <i>Streptococcus pyogenes</i> , SPs0871 and the development of a VHH inhibitor. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 565, 1-7	3.4	0

20	Mechanism of dimerization and structural features of human LI-cadherin. <i>Journal of Biological Chemistry</i> , 2021 , 297, 101054	5.4	○
19	Regulation of cadherin dimerization by chemical fragments as a trigger to inhibit cell adhesion. <i>Communications Biology</i> , 2021 , 4, 1041	6.7	○
18	Microsecond molecular dynamics suggest that a non-synonymous mutation, frequently observed in patients with mild symptoms in Tokyo, alters dynamics of the SARS-CoV-2 main protease. <i>Biophysics and Physicobiology</i> , 2021 , 18, 215-222	1.4	○
17	Addition of arginine hydrochloride and proline to the culture medium enhances recombinant protein expression in <i>Brevibacillus choshinensis</i> : The case of RBD of SARS-CoV-2 spike protein and its antibody.. <i>Protein Expression and Purification</i> , 2022 , 106075	2	○
16	Antibody recognition of complement Factor H reveals a flexible loop involved in Atypical Hemolytic Uremic Syndrome pathogenesis.. <i>Journal of Biological Chemistry</i> , 2022 , 101962	5.4	○
15	Development of a high-throughput method to screen novel antiviral materials.. <i>PLoS ONE</i> , 2022 , 17, e0266474	6.4	○
14	Formulation and Stability 2016 , 105-129		
13	Revealing the peptide presenting process of human leukocyte antigen through the analysis of fluctuation. <i>Biophysics (Nagoya-shi, Japan)</i> , 2015 , 11, 103-6		
12	2P120 SELEX experiments of a hyperthermostable TATA-box-binding protein at different temperatures(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008 , 48, S93		○
11	1P125 Thermodynamic profiles of the interaction between hyperthermostable TATA-box binding protein and a double-stranded DNA at high temperature(Protein engineering, evolutionary engineering, nucleic acid-binding proteins, and nucleic acid, Oral Presentations). <i>Seibutsu Butsuri</i> , 2007 , 47, S51		○
10	2P019 The solubility of amino acids, diglycine, triglycine in aqueous L-Arginine hydrochloride solution(29. Protein structure and dynamics (II), Poster Session, Abstract, Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , 2006 , 46, S300		○
9	Open Sandwich Selection: Selection of Human Antibody Fragments Using the Mechanism of Fv Fragment Stabilization in the Presence of Antigen. <i>ACS Symposium Series</i> , 2002 , 285-295		○.4
8	A Method for Efficient Refolding of Antibody Domains. <i>Seibutsu Butsuri</i> , 2000 , 40, 274-276		○
7	Application of Spectroscopic Folding Study to Highly Efficient Refolding Systems-With a Focus on Antibody Molecules-. <i>Seibutsu Butsuri</i> , 2004 , 44, 102-107		○
6	INTERACTION OF THE INNER EAR MOTOR PROTEIN PRESTIN WITH CHLORIDE STUDIED BY ISOTHERMAL TITRATION CALORIMETRY(2A1 Micro & Nano Biomechanics IV). <i>The Proceedings of the Asian Pacific Conference on Biomechanics Emerging Science and Technology in Biomechanics</i> , 2007 , 2007.3, S137		
5	MISFOLDING AND MISLOCALIZATION BY MUTATIONS OF THE MOTOR PROTEIN PRESTIN(2A1 Micro & Nano Biomechanics IV). <i>The Proceedings of the Asian Pacific Conference on Biomechanics Emerging Science and Technology in Biomechanics</i> , 2007 , 2007.3, S136		
4	Structural basis for selective inhibition of human serine hydroxymethyltransferase by secondary bile acid conjugate. <i>IScience</i> , 2021 , 24, 102036	6.1	
3	Single-chain variable fragment (scFv) targeting streptolysin O controls group A Streptococcus infection. <i>Biochemical and Biophysical Research Communications</i> , 2021 , 566, 177-183	3.4	

- 2 Electrostatic-triggered exothermic antibody adsorption to the cellulose nanoparticles. *Analytical Biochemistry*, **2021**, 632, 114337 3.1
- 1 Structure and role of the linker domain of the iron surface-determinant protein IsdH in heme transportation in *Staphylococcus aureus*.. *Journal of Biological Chemistry*, **2022**, 101995 5.4